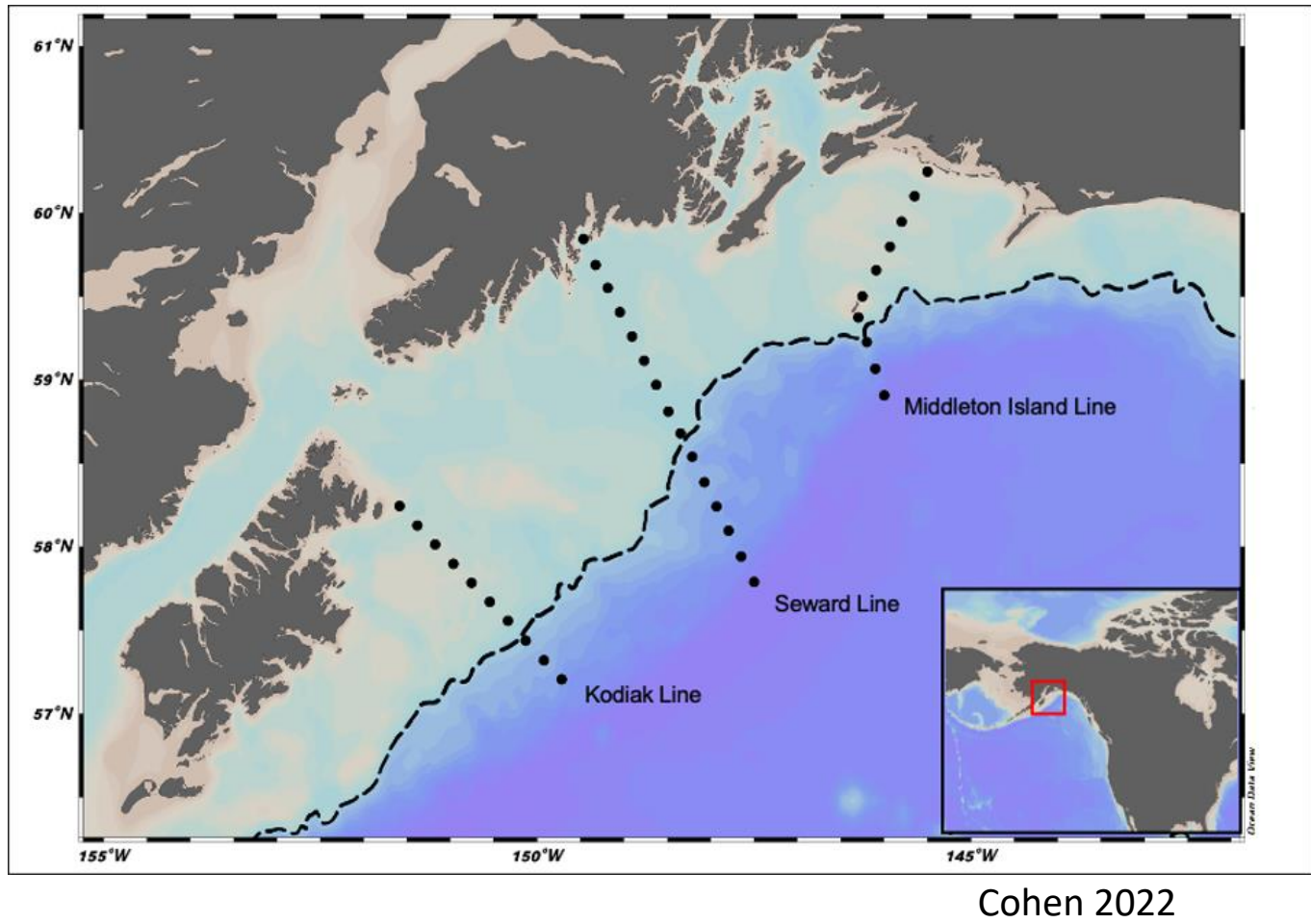


Co-occurrence networks of marine microbes in the Northern Gulf of Alaska

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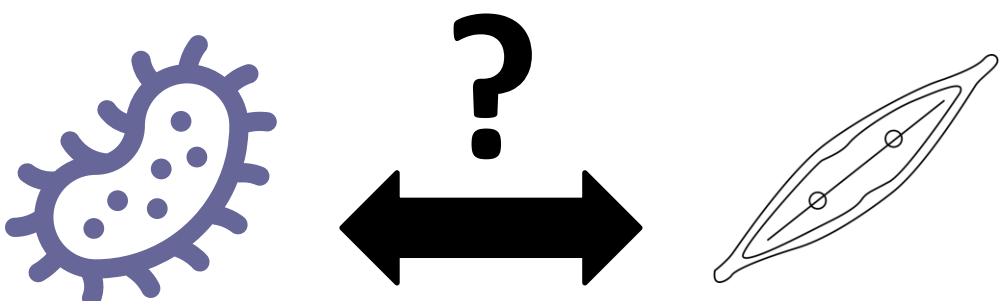
Introduction

- The Northern Gulf of Alaska (NGA) is a highly productive ecosystem with a diverse microbial community.
- Samples from summers 2018-2021 were sequenced for 16S (V4) and 18S (V9) rRNA.
- Interactions between microbes, both competitive and beneficial, likely shape this ecosystem.
- Co-occurrence networks allow us to begin understanding which microbes are sharing the same niche and potentially interacting with one another.

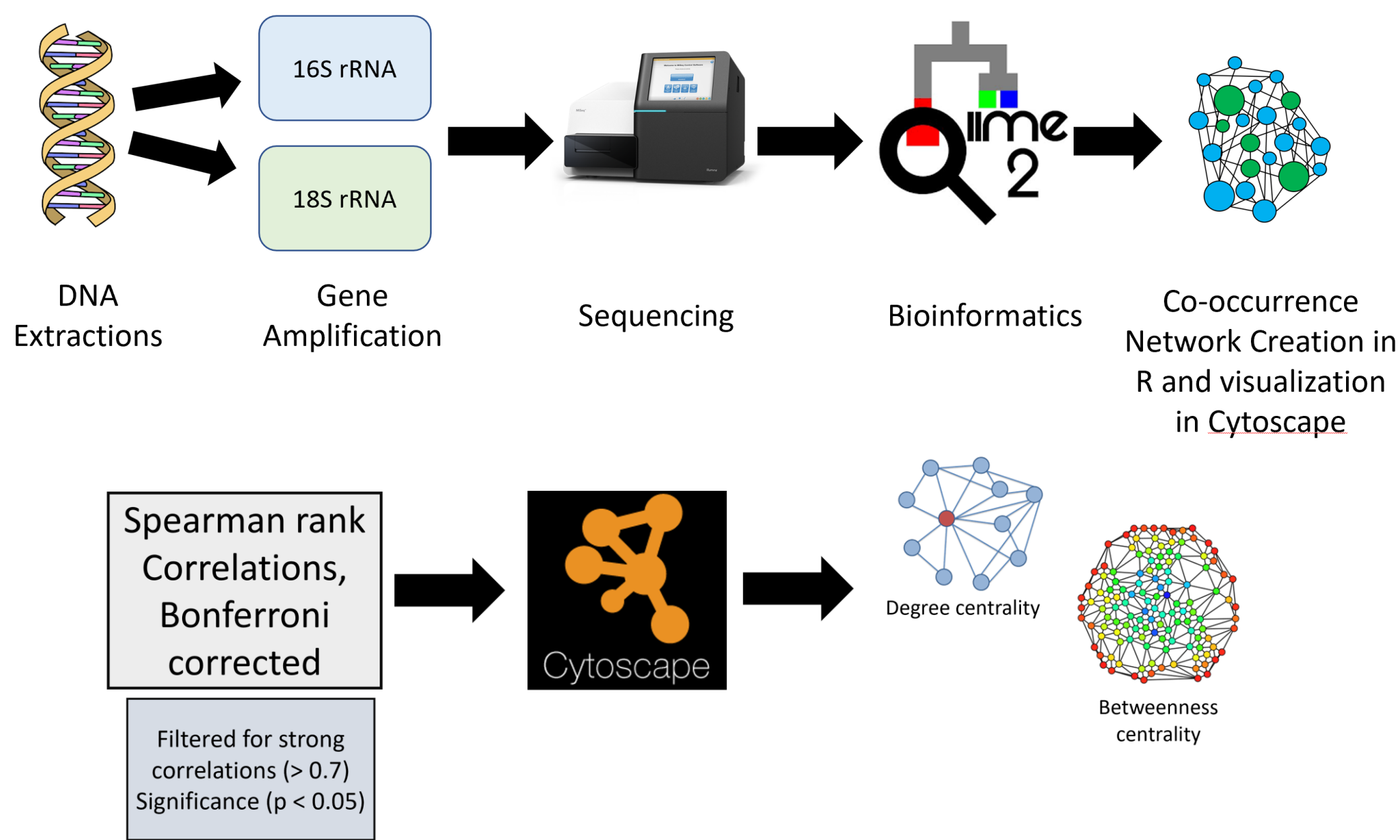


Big Question

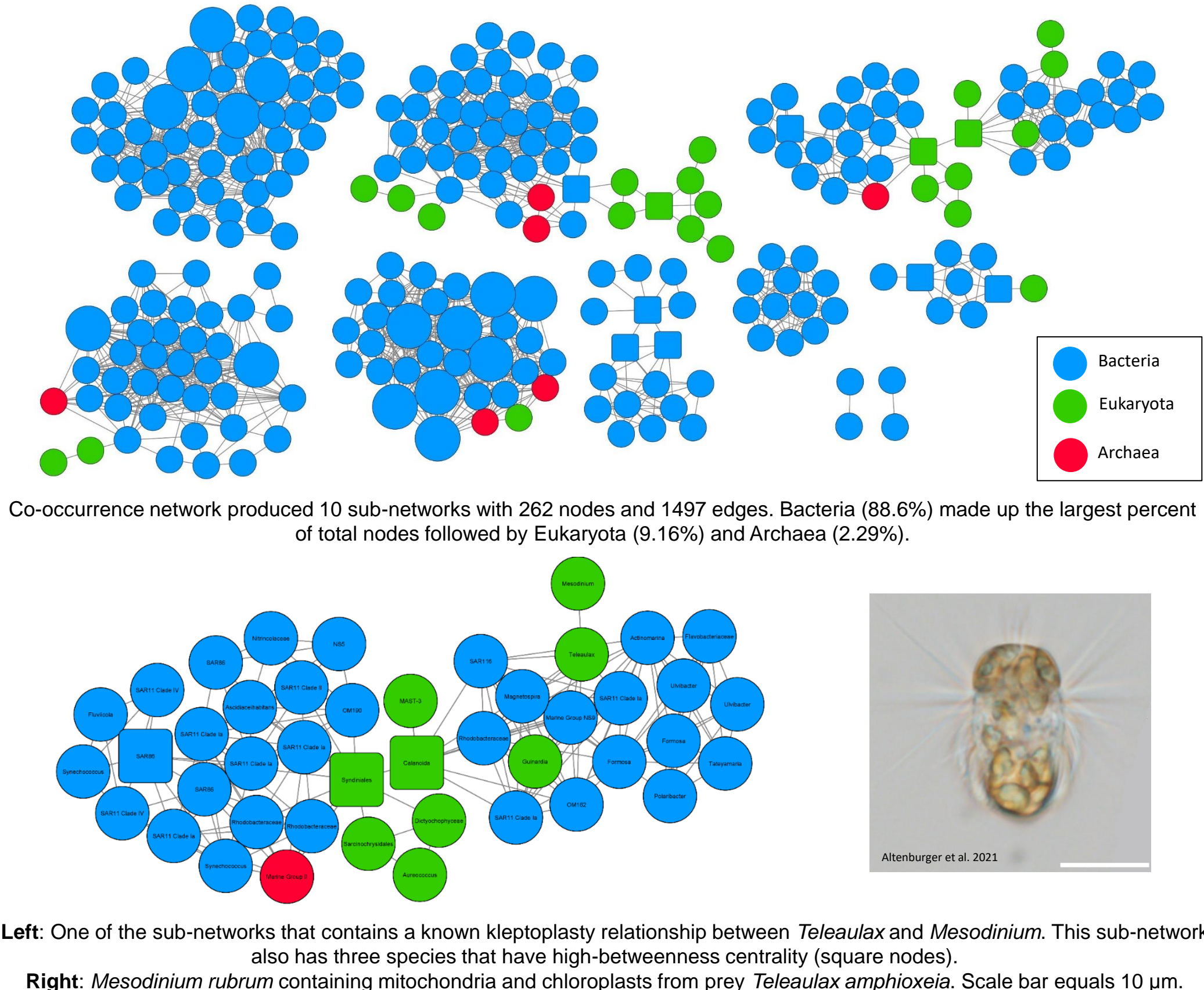
What are the potential microbial interactions and who are the key microbial players in the Northern Gulf of Alaska?



Methods

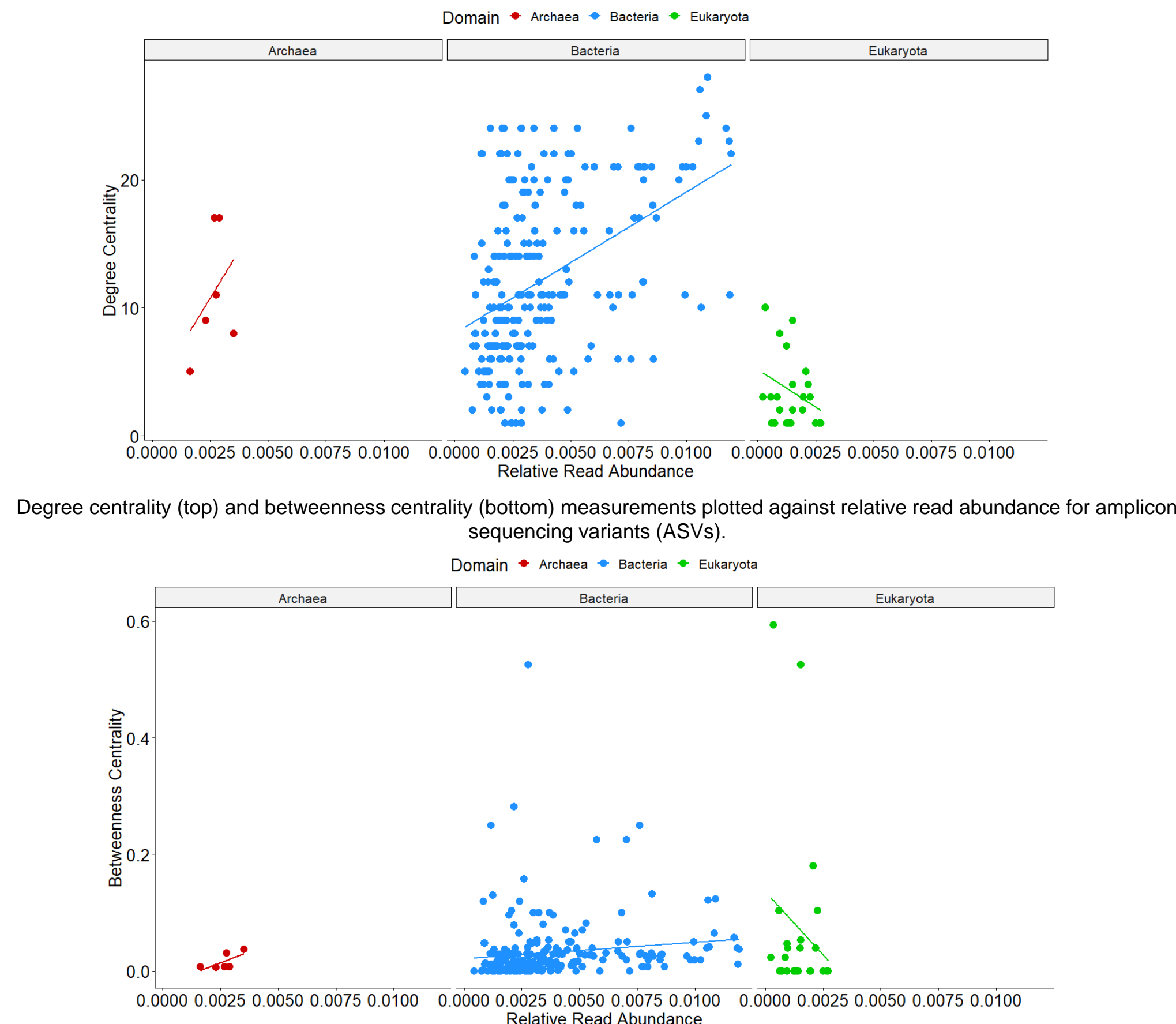


Co-occurrence Network

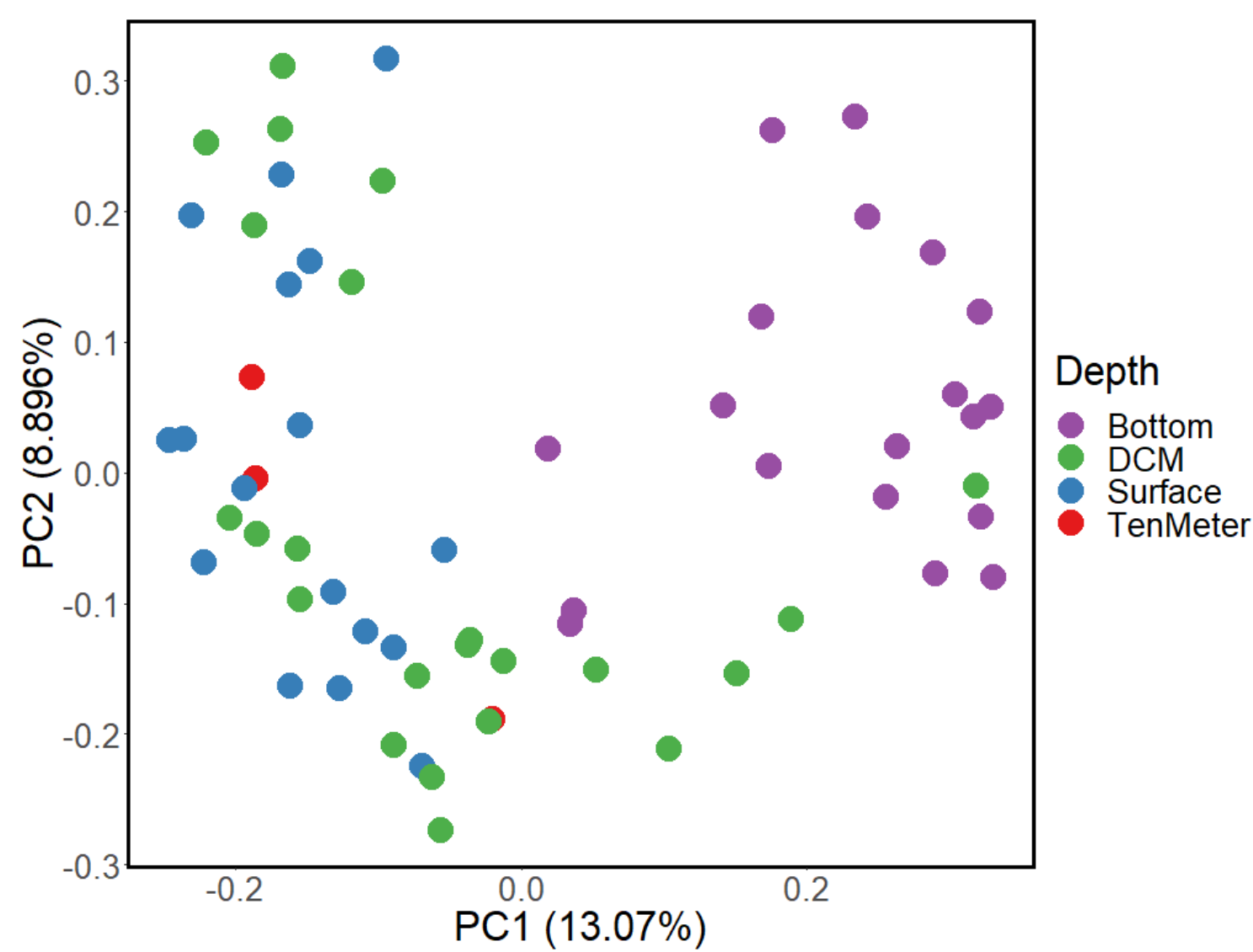


Left: One of the sub-networks that contains a known kleptoplasty relationship between *Teleaulax* and *Mesodinium*. This sub-network also has three species that have high-betweenness centrality (square nodes).
Right: *Mesodinium rubrum* containing mitochondria and chloroplasts from prey *Teleaulax amphioxeia*. Scale bar equals 10 μ m.

Abundance \neq Importance



Prokaryotic Community Differences



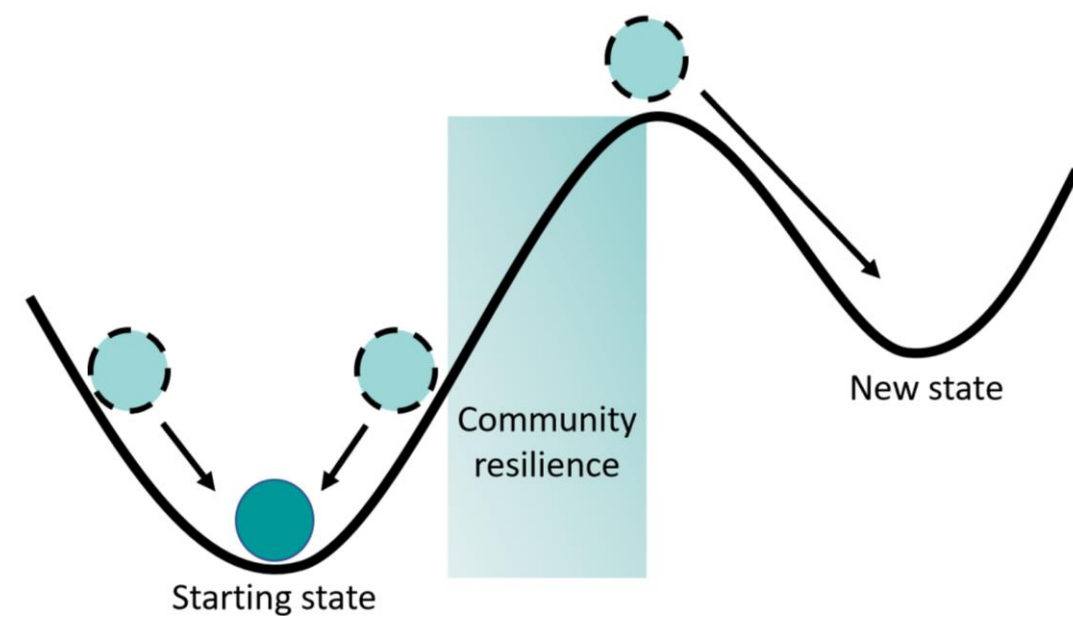
Principal coordinates analysis on the unweighted UniFrac distance matrix from rarefied taxa abundance and patterns of beta diversity for prokaryotic NGA water communities at different depths. Multiple Response Permutation Procedure (MRPP) between 16S communities and depth was significant ($p = 0.028$).

Discussion

- Co-occurrence networks produced significantly positive correlations between eukaryotes, archaea, and bacteria in NGA.
- Known interactions were recovered including a kleptoplastic ciliate and cryptophyte.
- Eukaryotes do not have to be highly abundant to be central in the co-occurrence network.
- We hypothesize that species with high degree and betweenness centrality could play a key role within the community and their removal could disproportionately affect community structure.
- Next steps are to investigate gene functionality using metagenomes and metatranscriptomes.

Implications

Important species within the system are not necessarily the most abundant but their removal could push the community toward a new state.



Acknowledgments

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